

Figure 1

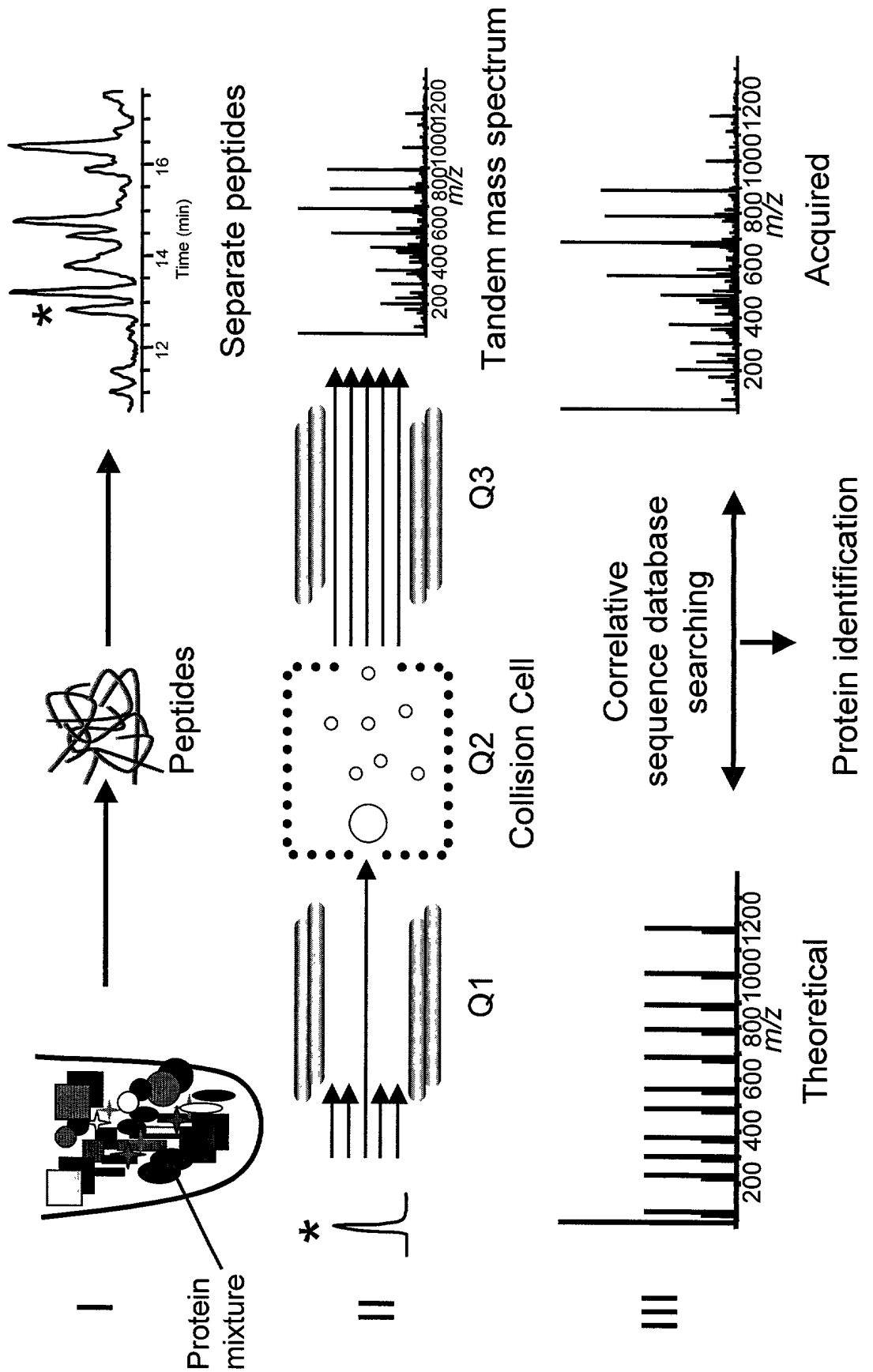
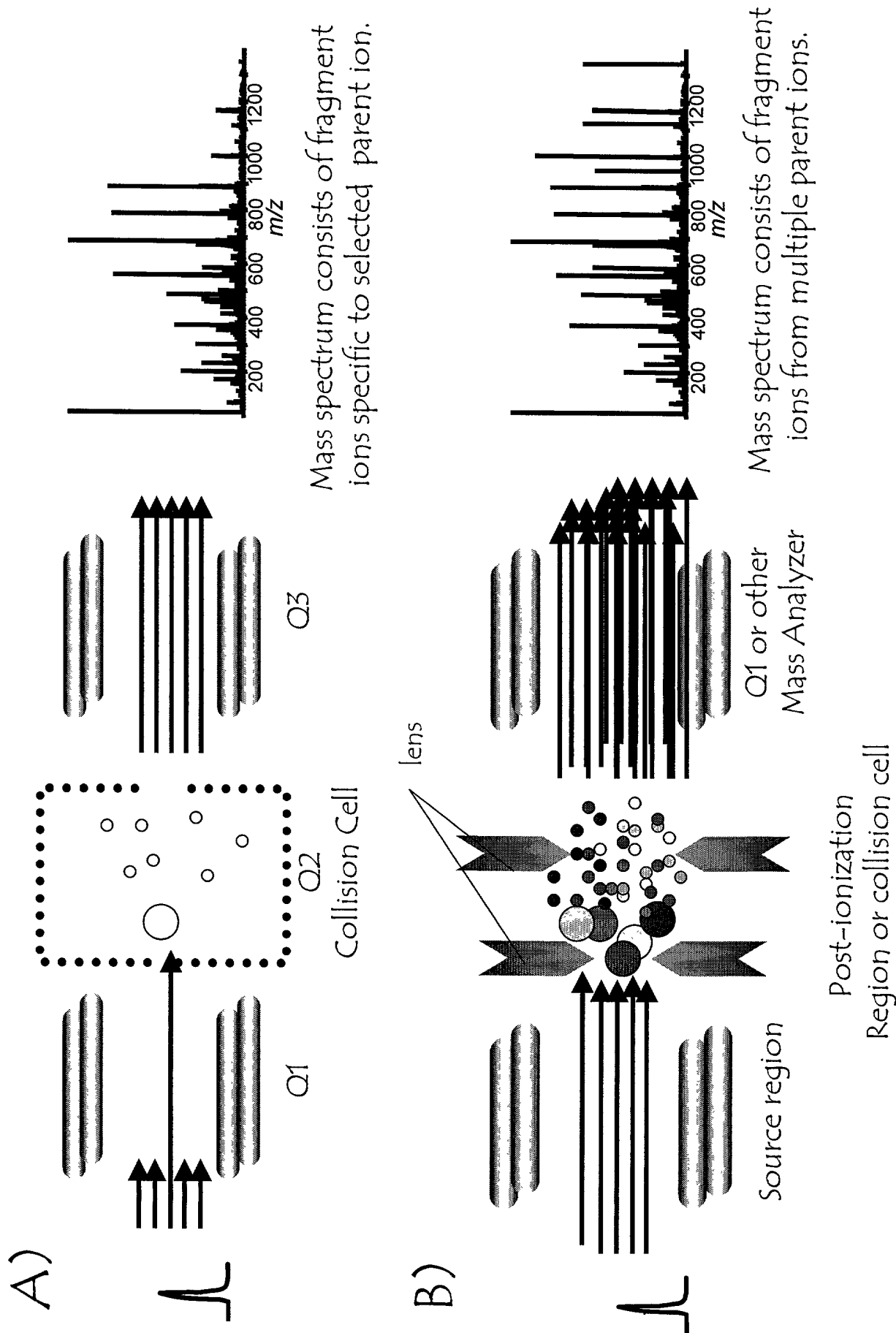


Figure 2



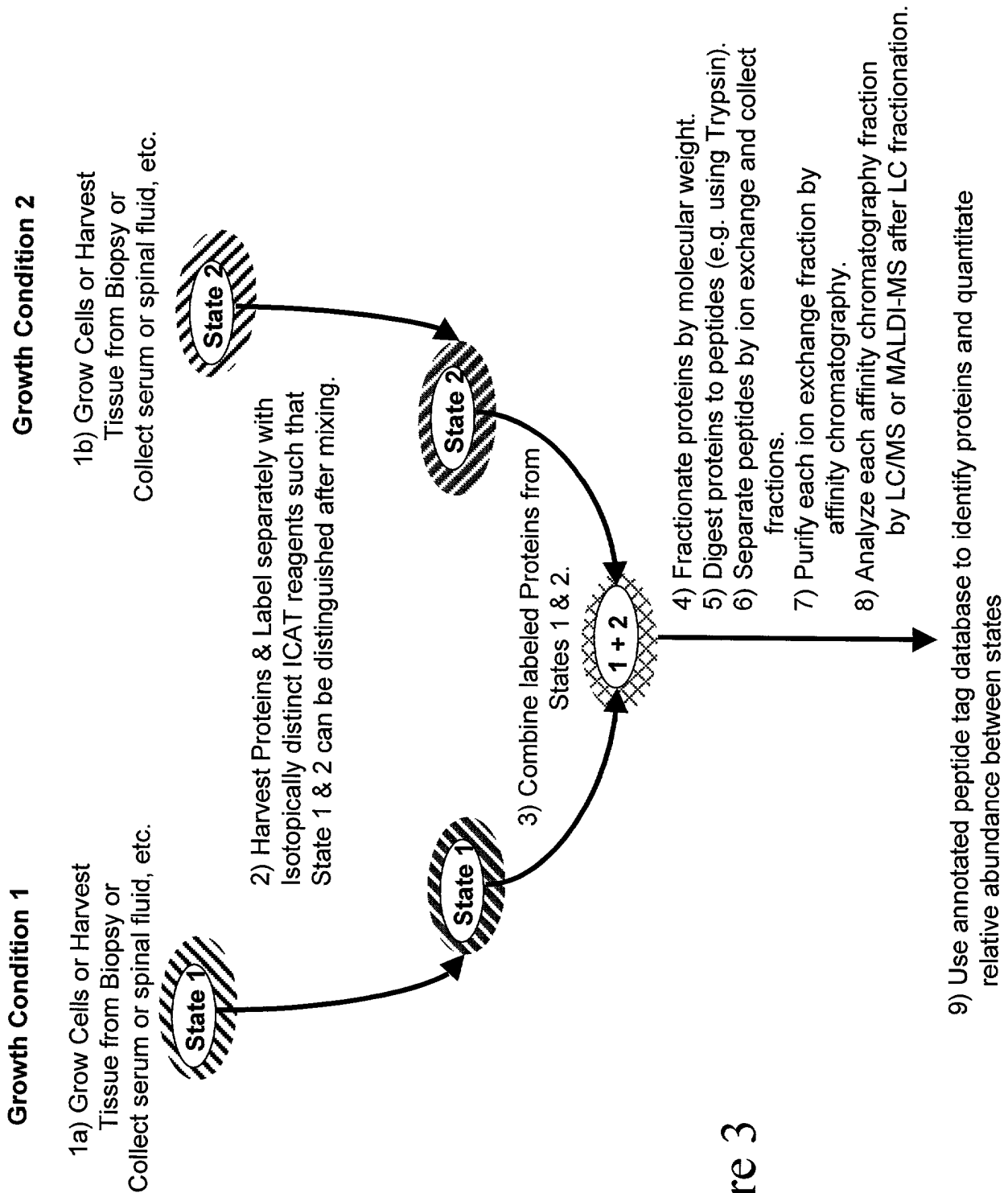
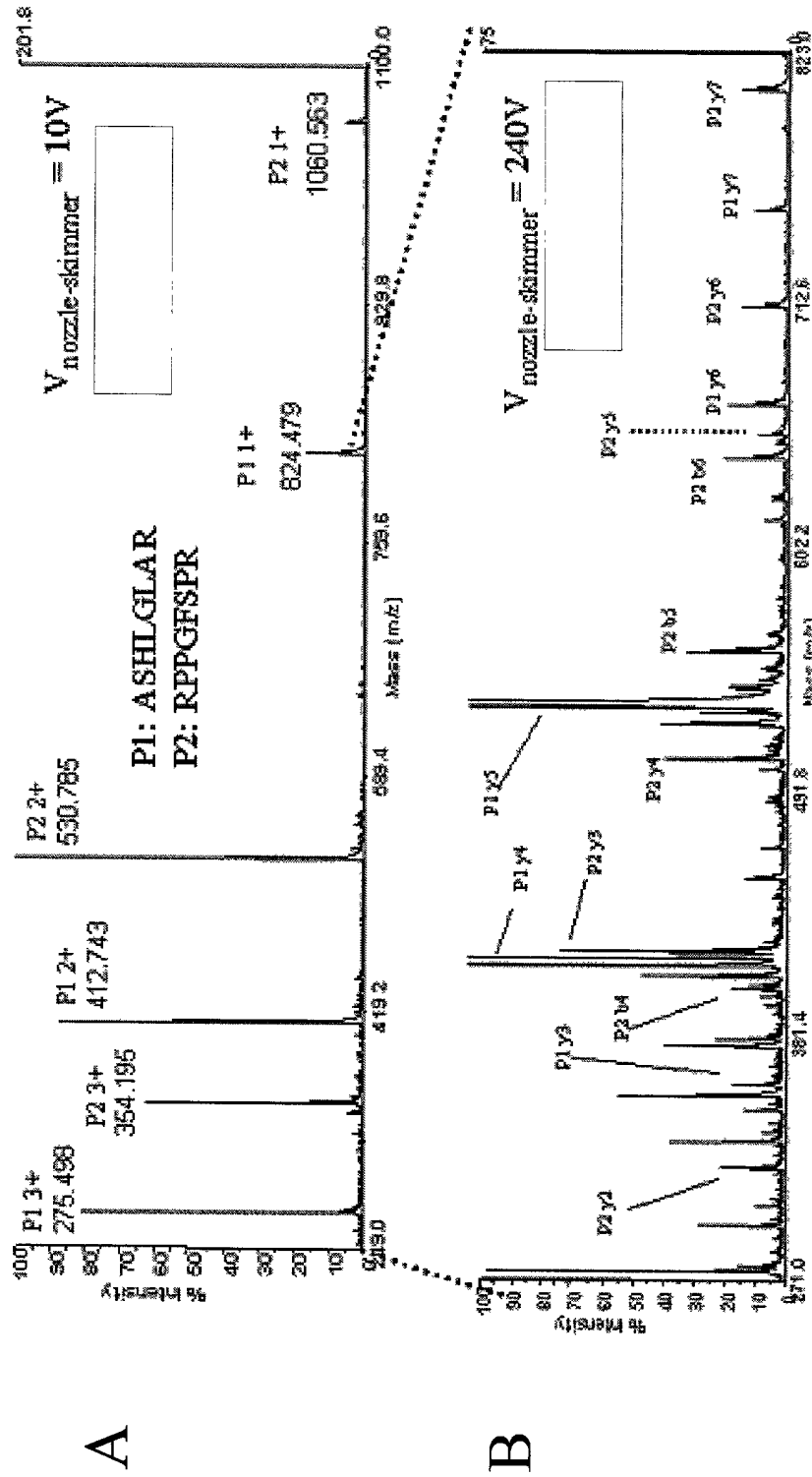


Figure 3

Figure 4



C

Human protein database:  
60,884 sequence entries

Fragment ion masses used for analysis:

710.385  
753.435  
807.374  
886.402  
904.451  
1001.564

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Bradykinin RPPGFSPFR MH+ 1060.5676

at 10 PPM, 144 tryptic peptides match

13 matches using fragment ion constraint:

ACISEILPSK  
GVRYSFGFK  
RANLISQCR  
RCGLPSSGKR  
RDITLEASR  
RERETLEK  
RLTEEERK  
RLVEVDSSR  
RNLLDHHR  
RPHAAQPGAR  
RPPGFSPFR \*\*  
RPQTATASTK  
RRPSAYQAL

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ASHLGLAR MH+ 824.4739

at 10PPM, 57 tryptic peptides match

12 matches using fragment ion constraint:

ACYIKVK  
ADPLPRR  
AFVAFAAK  
AFVFGRK  
AHAEIRK  
AHEAKIR  
ALEAHKR  
ALQFFAK  
AMAIYKK  
APDPRLR  
ASHLGLAR \*\*  
AVAGHLTR

Figure 4